ABSTRACT

Neural networks are constructed (programmed), and trained on historical data relating the (i) alleles, to the (ii) clinical responses, of a large number of patients. The trained neural networks show which alleles are, in combination, of practical pertinence to a wide range of biological, social and clinical variables. The trained neural networks may be exercised to predict (i) the responses of populations to different therapies, and (ii) the occurrences of adverse reactions. The trained neural networks are exercised in consideration of the genomic data of an individual patient to predict the response(s) of the individual patient to, most particularly usefully, any of (1) optimal drug dosage, (2) drug dosage sensitivity, (3) expected therapeutic outcome(s), and/or (4) adverse side effects may can be predicted in consideration of the alleles of the patient. Both the human and the economic costs of both optimal and sub-optimal drug therapies may be extrapolated from the exercise of various optimized and trained neural networks. The preferred neural network mapping is on (i) inputs that have underdone "householding", meaning that multiple genes are treated as a single unit, by (ii) use of a Genetic Algorithm (GA) that is "rolled", meaning that mapping transpires in neural networks organized hierarchically in stages so as to relate a typically vast amount genomic data as neural networks inputs to but very little clinical data as the outputs of a final, root node, neural network.